

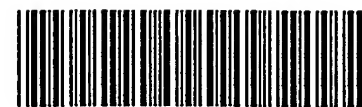
RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101524,979
Source: PCT
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PCT

RAW SEQUENCE LISTING

DATE: 03/08/2005

PATENT APPLICATION: US/10/524,979

TIME: 07:59:44

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\03082005\J524979.raw

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3 <110> APPLICANT: Takemori, Hiroshi
4     Okamoto, Mitsuhiro
6 <120> TITLE OF INVENTION: SALT-INDUCIBLE KINASE 2 AND USE THEREOF
8 <130> FILE REFERENCE: WATA-003
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/524,979
C--> 11 <141> CURRENT FILING DATE: 2005-02-18
11 <150> PRIOR APPLICATION NUMBER: 2002-240092
12 <151> PRIOR FILING DATE: 2002-08-21
14 <150> PRIOR APPLICATION NUMBER: 2003-23295
15 <151> PRIOR FILING DATE: 2003-01-31
17 <160> NUMBER OF SEQ ID NOS: 17
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2986
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
26 <400> SEQUENCE: 1
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29 aggcacttgc agcgcgggcc agtcggggtg gggttctacg acatcgaggg cacgctgggc 180
30 aagggcaact ttgccgtggt gaagctgggg cggcaccgga ccaccaagac ggaggtggct 240
31 ataaaaataa tagacaagtc acagctggat gcagtaaacc ttgagaaaat ctaccgagaa 300
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33 accaaaagta tgttgtagct tgtgacagaa tatgccaaaa atggagaaaat ttttgattat 420
34 cttgctaate atggccgatt aaatgaatct gaagccagga gaaaattctg gcaaattctg 480
35 tctgctgttg attattgcca tggccggaag gtagtgaca gagacctgaa ggctgaaaat 540
36 ctctgtctgg ataacaacat gaatatcaaa atagcagatt tcggcttttg aaatttcttt 600
37 aaaactggtg aactgctggc aacatggtgt ggcagccccc cttatgcagc ccagaagtc 660
38 tttgaagggc agcagtatga aggaccacag ctggatatat ggagcatggg agttgttctt 720
39 tatgtccttg tctgtggagc tctacctttt gatggacca ctctccctat tttgaggcag 780
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43 gaaaacgagc cgtccattgg agaatttaat gagcaggttc ttcgactgat gcacagcctt 1020
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53 gtgactaacc aattggttgt gatgccggg gcagggaaaa tgttctccat gagtgataac 1620
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55 tttctggaag acagcccttc cttgaaggac atcatgttag ccaatcagcc gtcaccccg 1740
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57 cagaagcgtg aggcccacaa ccggtccccc gtgagcttcc gagaaggccg cagagcatca 1860
58 gatacgtccc ttacacaagg aattgtggca tttagacaac atcttcagaa tcttgctaga 1920
59 accaaaggaa ttctggagtt gaacaaagta caattgctgt atgaacaaat gggatcaaac 1980
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61 caggaggaaa tctcccagca gcaggaaagt gtctccagcc tgtctgccag catgcacct 2100
62 cagctctcac cacagcaaag cttggaaacc cagtacctac agcatcgact ccagaagccc 2160
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75 gcccgggaga cctagcagct atggcaggac agttaggcaa cagatgaggg gctgcggaga 2940
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79 <210> SEQ ID NO: 2

80 <211> LENGTH: 931

81 <212> TYPE: PRT

82 <213> ORGANISM: Mus musculus

84 <400> SEQUENCE: 2

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88 Val Gly Phe Tyr Asp Ile Glu Gly Thr Leu Gly Lys Gly Asn Phe Ala
89             20             25             30
91 Val Val Lys Leu Gly Arg His Arg Thr Thr Lys Thr Glu Val Ala Ile
92             35             40             45
94 Lys Ile Ile Asp Lys Ser Gln Leu Asp Ala Val Asn Leu Glu Lys Ile
95             50             55             60
97 Tyr Arg Glu Val Gln Ile Met Lys Met Leu Asp His Pro His Ile Ile
98   65             70             75             80
100 Lys Leu Tyr Gln Val Met Glu Thr Lys Ser Met Leu Tyr Leu Val Thr
101             85             90             95
103 Glu Tyr Ala Lys Asn Gly Glu Ile Phe Asp Tyr Leu Ala Asn His Gly
104             100            105            110
106 Arg Leu Asn Glu Ser Glu Ala Arg Arg Lys Phe Trp Gln Ile Leu Ser
107             115            120            125
109 Ala Val Asp Tyr Cys His Gly Arg Lys Val Val His Arg Asp Leu Lys
110             130            135            140
112 Ala Glu Asn Leu Leu Leu Asp Asn Asn Met Asn Ile Lys Ile Ala Asp
113 145             150             155             160

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118 Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Val Phe Glu Gly Gln Gln
119                               180                               185                               190
121 Tyr Glu Gly Pro Gln Leu Asp Ile Trp Ser Met Gly Val Val Leu Tyr
122                               195                               200                               205
124 Val Leu Val Cys Gly Ala Leu Pro Phe Asp Gly Pro Thr Leu Pro Ile
125                               210                               215                               220
127 Leu Arg Gln Arg Val Leu Glu Gly Arg Phe Arg Ile Pro Tyr Phe Met
128 225                               230                               235                               240
130 Ser Glu Asp Cys Glu His Leu Ile Arg Arg Met Leu Val Leu Asp Pro
131                               245                               250                               255
133 Ser Lys Arg Leu Ser Ile Ala Gln Ile Lys Glu His Lys Trp Met Leu
134                               260                               265                               270
136 Ile Glu Val Pro Val Gln Arg Pro Ile Leu Tyr Pro Gln Glu Gln Glu
137                               275                               280                               285
139 Asn Glu Pro Ser Ile Gly Glu Phe Asn Glu Gln Val Leu Arg Leu Met
140                               290                               295                               300
142 His Ser Leu Gly Ile Asp Gln Gln Lys Thr Val Glu Ser Leu Gln Asn
143 305                               310                               315                               320
145 Lys Ser Tyr Asn His Phe Ala Ala Ile Tyr Phe Leu Leu Val Glu Arg
146                               325                               330                               335
148 Leu Lys Ser His Arg Ser Ser Phe Pro Val Glu Gln Arg Leu Asp Gly
149                               340                               345                               350
151 Arg Gln Arg Arg Pro Ser Thr Ile Ala Glu Gln Thr Val Ala Lys Ala
152                               355                               360                               365
154 Gln Thr Val Gly Leu Pro Val Thr Leu His Pro Pro Asn Val Arg Leu
155                               370                               375                               380
157 Met Arg Ser Thr Leu Leu Pro Gln Ala Ser Asn Val Glu Ala Phe Ser
158 385                               390                               395                               400
160 Phe Pro Thr Ser Ser Cys Gln Ala Glu Ala Ala Phe Met Glu Glu Glu
161                               405                               410                               415
163 Cys Val Asp Thr Pro Lys Val Asn Gly Cys Leu Leu Asp Pro Val Pro
164                               420                               425                               430
166 Pro Val Leu Val Arg Lys Gly Cys Gln Ser Leu Pro Ser Ser Met Met
167                               435                               440                               445
169 Glu Thr Ser Ile Asp Glu Gly Leu Glu Thr Glu Gly Glu Ala Glu Glu
170                               450                               455                               460
172 Asp Pro Ser Gln Ala Phe Glu Ala Phe Gln Ala Thr Arg Ser Gly Gln
173 465                               470                               475                               480
175 Arg Arg His Thr Leu Ser Glu Val Thr Asn Gln Leu Val Val Met Pro
176                               485                               490                               495
178 Gly Ala Gly Lys Met Phe Ser Met Ser Asp Asn Pro Ser Leu Glu Ser
179                               500                               505                               510
181 Val Asp Ser Glu Tyr Asp Met Gly Ser Ala Gln Arg Asp Leu Asn Phe
182                               515                               520                               525
184 Leu Glu Asp Ser Pro Ser Leu Lys Asp Ile Met Leu Ala Asn Gln Pro
185                               530                               535                               540
187 Ser Pro Arg Met Thr Ser Pro Phe Ile Ser Leu Arg Pro Ala Asn Pro

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194          580          585          590
196 Gln Gly Ile Val Ala Phe Arg Gln His Leu Gln Asn Leu Ala Arg Thr
197          595          600          605
199 Lys Gly Ile Leu Glu Leu Asn Lys Val Gln Leu Leu Tyr Glu Gln Met
200          610          615          620
202 Gly Ser Asn Ala Asp Pro Thr Leu Thr Ser Thr Ala Pro Gln Leu Gln
203 625          630          635          640
205 Asp Leu Ser Ser Ser Cys Pro Gln Glu Glu Ile Ser Gln Gln Gln Glu
206          645          650          655
208 Ser Val Ser Ser Leu Ser Ala Ser Met His Pro Gln Leu Ser Pro Gln
209          660          665          670
211 Gln Ser Leu Glu Thr Gln Tyr Leu Gln His Arg Leu Gln Lys Pro Asn
212          675          680          685
214 Leu Leu Pro Lys Ala Gln Ser Pro Cys Pro Val Tyr Cys Lys Glu Pro
215          690          695          700
217 Pro Arg Ser Leu Glu Gln Gln Leu Gln Glu His Arg Leu Gln Gln Lys
218 705          710          715          720
220 Arg Leu Phe Leu Gln Lys Gln Ser Gln Leu Gln Ala Tyr Phe Asn Gln
221          725          730          735
223 Met Gln Ile Ala Glu Ser Ser Tyr Pro Gly Pro Ser Gln Gln Leu Ala
224          740          745          750
226 Leu Pro His Gln Glu Thr Pro Leu Thr Ser Gln Gln Pro Pro Ser Phe
227          755          760          765
229 Ser Leu Thr Gln Ala Leu Ser Pro Val Leu Glu Pro Ser Ser Glu Gln
230          770          775          780
232 Met Gln Phe Ser Ser Phe Leu Ser Gln Tyr Pro Glu Met Gln Leu Gln
233 785          790          795          800
235 Pro Leu Pro Ser Thr Pro Gly Pro Arg Ala Pro Pro Pro Leu Pro Ser
236          805          810          815
238 Gln Leu Gln Gln His Gln Gln Pro Pro Pro Pro Pro Pro Pro Pro
239          820          825          830
241 Pro Gln Gln Pro Gly Ala Ala Pro Thr Ser Leu Gln Phe Ser Tyr Gln
242          835          840          845
244 Thr Cys Glu Leu Pro Ser Thr Thr Ser Ser Val Pro Asn Tyr Pro Ala
245          850          855          860
247 Ser Cys His Tyr Pro Val Asp Gly Ala Gln Gln Ser Asn Leu Thr Gly
248 865          870          875          880
250 Ala Asp Cys Pro Arg Ser Ser Gly Leu Gln Asp Thr Ala Ser Ser Tyr
251          885          890          895
253 Asp Pro Leu Ala Leu Ser Glu Leu Pro Gly Leu Phe Asp Cys Glu Met
254          900          905          910
256 Val Glu Ala Val Asp Pro Gln His Asn Gly Val Val Ser Cys Leu Ala
257          915          920          925
259 Arg Glu Thr
260          930

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264 <211> LENGTH: 141
265 <212> TYPE: DNA
266 <213> ORGANISM: Mus musculus
268 <400> SEQUENCE: 3
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270 gcatttagac aacatcttca gaatcttgct agaaccaaag gaattctgga gttgaacaaa 120
271 gtacaattgc tgtatgaaca a                                     141
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275 <211> LENGTH: 47
276 <212> TYPE: PRT
277 <213> ORGANISM: Mus musculus
279 <400> SEQUENCE: 4
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283 Gln Gly Ile Val Ala Phe Arg Gln His Leu Gln Asn Leu Ala Arg Thr
284           20           25           30
286 Lys Gly Ile Leu Glu Leu Asn Lys Val Gln Leu Leu Tyr Glu Gln
287   35           40           45
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291 <211> LENGTH: 756
292 <212> TYPE: DNA
293 <213> ORGANISM: Mus musculus
295 <400> SEQUENCE: 5
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298 aacottgaga aaatctaccg agaagtacag ataatgaaaa tgctcgacca tcctcacatc 180
299 attaaactgt atcaggtaat ggagacaaaa agtatgttgt acctgtgac agaatatgcc 240
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306 ccaactctcc ctatttttgag gcagagggtt ttagaaggaa gattccggat tccttatttc 660
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308 ctaagcatag ctcaaataca ggagcacaag tggatg                                     756
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312 <211> LENGTH: 252
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314 <213> ORGANISM: Mus musculus
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321           20           25           30
323 Asp Lys Ser Gln Leu Asp Ala Val Asn Leu Glu Lys Ile Tyr Arg Glu
324           35           40           45
326 Val Gln Ile Met Lys Met Leu Asp His Pro His Ile Ile Lys Leu Tyr

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VERIFICATION SUMMARY

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Input Set : E:\seqlist.txt

Output Set: N:\CRF4\03082005\J524979.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date